

SEQUENCE LISTING

<110> CHEUNG, WING Y.
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LAFOREST, MARTIN
LANDRY, BENOIT S.

<120> COMPOSITIONS AND METHODS FOR IDENTIFYING PLANTS HAVING
INCREASED TOLERANCE TO IMIDAZOLINONE HERBICIDES

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<170> PatentIn Ver. 3.2

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gta gag aat ctt cct gtg aag ata ctc ttg tta aac aac cag cat ctt	1683
Val Glu Asn Leu Pro Val Lys Ile Leu Leu Leu Asn Asn Gln His Leu	
540 545 550	
ggg atg gtc atg caa tgg gaa gat cgg ttc tac aaa gct aac aga gct	1731
Gly Met Val Met Gln Trp Glu Asp Arg Phe Tyr Lys Ala Asn Arg Ala	
555 560 565	
cac act tat ctc ggg gac ccg gca agg gag aac gag atc ttc cct aac	1779
His Thr Tyr Leu Gly Asp Pro Ala Arg Glu Asn Glu Ile Phe Pro Asn	
570 575 580 585	
atg ctg cag ttt gca gga gct tgc ggg att cca gct gcg aga gtg acg	1827
Met Leu Gln Phe Ala Gly Ala Cys Gly Ile Pro Ala Ala Arg Val Thr	
590 595 600	
aag aaa gaa gaa ctc cga gaa gct att cag aca atg ctg gat aca cca	1875
Lys Lys Glu Glu Leu Arg Glu Ala Ile Gln Thr Met Leu Asp Thr Pro	
605 610 615	
gga cca tac ctg ttg gat gtg ata tgt ccg cac caa gaa cat gtg tta	1923
Gly Pro Tyr Leu Leu Asp Val Ile Cys Pro His Gln Glu His Val Leu	
620 625 630	
ccg atg atc cca agt ggt ggc act ttc aaa gat gta ata aca gaa ggg	1971
Pro Met Ile Pro Ser Gly Gly Thr Phe Lys Asp Val Ile Thr Glu Gly	
635 640 645	
gat ggt cgc act aag tac tgagagatga agctgggtgat cgatcatatg	2019
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ttgt	2083

—

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Thr	Ser	Pro	Ser	Pro	Ile	Ser	Leu	Thr	Ala	Lys	Pro	Ser	Ser	Lys	Ser	
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cct	cta	ccc	att	tcc	aga	ttc	tcc	ctt	ccc	ttc	tcc	tta	acc	cca	cag	150
Pro	Leu	Pro	Ile	Ser	Arg	Phe	Ser	Leu	Pro	Phe	Ser	Leu	Thr	Pro	Gln	
				25					30					35		
aaa	ccc	tcc	tcc	cgt	ctc	cac	cgt	cca	ctc	gcc	atc	tcc	gcc	gtt	ctc	198
Lys	Pro	Ser	Ser	Arg	Leu	His	Arg	Pro	Leu	Ala	Ile	Ser	Ala	Val	Leu	
			40					45					50			
aac	tca	ccc	gtc	aat	gtc	gca	cct	gaa	aaa	acc	gac	aag	atc	aag	act	246
Asn	Ser	Pro	Val	Asn	Val	Ala	Pro	Glu	Lys	Thr	Asp	Lys	Ile	Lys	Thr	
		55					60					65				
ttc	atc	tcc	cgc	tac	gct	ccc	gac	gag	ccc	cgc	aag	ggg	gct	gat	atc	294
Phe	Ile	Ser	Arg	Tyr	Ala	Pro	Asp	Glu	Pro	Arg	Lys	Gly	Ala	Asp	Ile	
	70					75					80					
ctc	gtg	gaa	gcc	ctc	gag	cgt	caa	ggc	gtc	gaa	acc	gtc	ttc	gct	tat	342
Leu	Val	Glu	Ala	Leu	Glu	Arg	Gln	Gly	Val	Glu	Thr	Val	Phe	Ala	Tyr	
85					90					95					100	
ccc	gga	ggg	gcc	tcc	atg	gag	atc	cac	caa	gcc	ttg	act	cgc	tcc	tcc	390
Pro	Gly	Gly	Ala	Ser	Met	Glu	Ile	His	Gln	Ala	Leu	Thr	Arg	Ser	Ser	
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acc	atc	cgt	aac	gtc	ctc	ccc	cgt	cac	gaa	caa	gga	gga	gtc	ttc	gcc	438
Thr	Ile	Arg	Asn	Val	Leu	Pro	Arg	His	Glu	Gln	Gly	Gly	Val	Phe	Ala	
			120					125					130			
gcc	gag	ggg	tac	gct	cgt	tcc	tcc	ggc	aaa	ccg	gga	atc	tgc	ata	gcc	486
Ala	Glu	Gly	Tyr	Ala	Arg	Ser	Ser	Gly	Lys	Pro	Gly	Ile	Cys	Ile	Ala	
		135					140					145				

act tcg ggt ccc gga gct acc aac ctc gtc agc ggg tta gcc gac gcg	534
Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Ser Gly Leu Ala Asp Ala	
150 155 160	
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Met Leu Asp Ser Val Pro Leu Val Ala Ile Thr Gly Gln Val Pro Arg	
165 170 175 180	
cgg atg atc ggt act gac gcg ttc caa gag acg cca atc gtt gag gta	630
Arg Met Ile Gly Thr Asp Ala Phe Gln Glu Thr Pro Ile Val Glu Val	
185 190 195	
acg agg tct att acg aaa cat aac tat ctg gtg atg gat gtt gat gac	678
Thr Arg Ser Ile Thr Lys His Asn Tyr Leu Val Met Asp Val Asp Asp	
200 205 210	
ata cct agg atc gtt caa gaa gca ttc ttt cta gct act tcc ggt aga	726
Ile Pro Arg Ile Val Gln Glu Ala Phe Phe Leu Ala Thr Ser Gly Arg	
215 220 225	
ccc gga ccg gtt ttg gtt gat gtt cct aag gat att cag cag cag ctt	774
Pro Gly Pro Val Leu Val Asp Val Pro Lys Asp Ile Gln Gln Gln Leu	
230 235 240	
gcg att cct aac tgg gat caa cct atg cgc ttg cct ggc tac atg tct	822
Ala Ile Pro Asn Trp Asp Gln Pro Met Arg Leu Pro Gly Tyr Met Ser	
245 250 255 260	
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Arg Leu Pro Gln Pro Pro Glu Val Ser Gln Leu Gly Gln Ile Val Arg	
265 270 275	
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Leu Ile Ser Glu Ser Lys Arg Pro Val Leu Tyr Val Gly Gly Gly Ser	
280 285 290	
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Leu Asn Ser Ser Glu Glu Leu Gly Arg Phe Val Glu Leu Thr Gly Ile	
295 300 305	
cct gtt gcg agt acg ttg atg ggg ctt ggc tct tat cct tgt aac gat	1014
Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ser Tyr Pro Cys Asn Asp	
310 315 320	
gag ttg tcc ctg cag atg ctt ggc atg cac ggg act gtg tat gct aac	1062
Glu Leu Ser Leu Gln Met Leu Gly Met His Gly Thr Val Tyr Ala Asn	
325 330 335 340	
tac gct gtg gag cat agt gat ttg ttg ctg gcg ttt ggt gtt agg ttt	1110
Tyr Ala Val Glu His Ser Asp Leu Leu Leu Ala Phe Gly Val Arg Phe	
345 350 355	

gat gac cgt gtc acg gga aag ctc gag gcg ttt gcg agc agg gct aag	1158
Asp Asp Arg Val Thr Gly Lys Leu Glu Ala Phe Ala Ser Arg Ala Lys	
360 365 370	
att gtg cac ata gac att gat tct gct gag att ggg aag aat aag aca	1206
Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly Lys Asn Lys Thr	
375 380 385	
cct cac gtg tct gtg tgt ggt gat gta aag ctg gct ttg caa ggg atg	1254
Pro His Val Ser Val Cys Gly Asp Val Lys Leu Ala Leu Gln Gly Met	
390 395 400	
aac aag gtt ctt gag aac cgg gcg gag gag ctc aag ctt gat ttc ggt	1302
Asn Lys Val Leu Glu Asn Arg Ala Glu Glu Leu Lys Leu Asp Phe Gly	
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Val Trp Arg Ser Glu Leu Ser Glu Gln Lys Gln Lys Phe Pro Leu Ser	
425 430 435	
ttc aaa acg ttt gga gaa gcc att cct ccg cag tac gcg att cag gtc	1398
Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro Gln Tyr Ala Ile Gln Val	
440 445 450	
cta gac gag cta acc caa ggg aag gca att atc agt act ggt gtt gga	1446
Leu Asp Glu Leu Thr Gln Gly Lys Ala Ile Ile Ser Thr Gly Val Gly	
455 460 465	
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Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr Arg Lys Pro Arg	
470 475 480	
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Gln Trp Leu Ser Ser Ser Gly Leu Gly Ala Met Gly Phe Gly Leu Pro	
485 490 495 500	
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Ala Ala Ile Gly Ala Ser Val Ala Asn Pro Asp Ala Ile Val Val Asp	
505 510 515	
att gac ggt gat gga agc ttc ata atg aac gtt caa gag ctg gcc aca	1638
Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln Glu Leu Ala Thr	
520 525 530	
atc cgt gta gag aat ctt cct gtg aag ata ctc ttg tta aac aac cag	1686
Ile Arg Val Glu Asn Leu Pro Val Lys Ile Leu Leu Leu Asn Asn Gln	
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cat ctt ggg atg gtc atg caa tgg gaa gat cgg ttc tac aaa gct aac	1734
His Leu Gly Met Val Met Gln Trp Glu Asp Arg Phe Tyr Lys Ala Asn	
550 555 560	

aga gct cac act tat ctc ggg gac ccg gca agg gag aac gag atc ttc 1782
 Arg Ala His Thr Tyr Leu Gly Asp Pro Ala Arg Glu Asn Glu Ile Phe
 565 570 575 580

cct aac atg ctg cag ttt gca gga gct tgc ggg att cca gct gcg aga 1830
 Pro Asn Met Leu Gln Phe Ala Gly Ala Cys Gly Ile Pro Ala Ala Arg
 585 590 595

gtg acg aag aaa gaa gaa ctc cga gaa gct att cag aca atg ctg gat 1878
 Val Thr Lys Lys Glu Glu Leu Arg Glu Ala Ile Gln Thr Met Leu Asp
 600 605 610

aca cct gga ccg tac ctg ttg gat gtc atc tgt ccg cac caa gaa cat 1926
 Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile Cys Pro His Gln Glu His
 615 620 625

gtg tta ccg atg atc cca agt ggt ggc act ttc gaa gat gta ata acc 1974
 Val Leu Pro Met Ile Pro Ser Gly Gly Thr Phe Glu Asp Val Ile Thr
 630 635 640

gaa ggg gat ggt cgc act aag tac tgagagatga agctggtgat ccatcatatg 2028
 Glu Gly Asp Gly Arg Thr Lys Tyr
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<210> 8
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<400> 8
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<210> 9
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oligonucleotide

<400> 9
aacatgctgc agtttgcagg 20

<210> 10
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oligonucleotide

<400> 10
agtttgcagg agcttgcggg 20

<210> 11
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oligonucleotide

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oligonucleotide

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<210> 13
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oligonucleotide

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<210> 14
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<400> 15
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<210> 17
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oligonucleotide

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<210> 18
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<400> 18
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<210> 19
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<210> 20
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<210> 21
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<400> 25
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<210> 26
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<400> 26
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oligonucleotide

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<210> 29
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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<210> 30
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<223> Description of Artificial Sequence: Synthetic
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<210> 31
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<210> 33
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<400> 33
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<210> 34
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<400> 34
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<210> 35
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oligonucleotide

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ccaaattacc acacaaaaga 20

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oligonucleotide

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actgacaaac ccaaattacc 20

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<210> 38
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oligonucleotide

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<210> 39
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<210> 40
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<210> 41
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<210> 42
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<400> 42
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<210> 43
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<210> 44
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oligonucleotide

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<210> 45
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oligonucleotide

<400> 45
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<210> 46
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oligonucleotide

<400> 46
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<210> 47
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<210> 48
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<400> 48
ggagctatgg gtttcggact 20

<210> 49
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oligonucleotide

<400> 49
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<210> 50
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oligonucleotide

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tcctgctgcg attggagcgt 20

<210> 51
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<400> 51
attggagcgt ctgtggcgaa 20

<210> 52
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oligonucleotide

<400> 52
ctgtggcgaa ccctgatgcg 20

<210> 53
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<400> 53
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<210> 54
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oligonucleotide

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<210> 55
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oligonucleotide

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<210> 56
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oligonucleotide

<400> 56
tgatggaagc ttcataatga 20

<210> 57
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oligonucleotide

<400> 57
ttcataatga acgttcaaga 20

<210> 58
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 58
acgttcaaga gctggccaca 20

<210> 59
<211> 20
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 59
gctggccaca atccgtgtag

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<210> 60
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 60
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<210> 61
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 61
agaatcttcc tgtgaagata

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<210> 62
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 62
tgtgaagata ctcttgtaa

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<210> 63
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oligonucleotide

<400> 63
ctcttggttaa acaaccagca

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<210> 64
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 64
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<210> 65
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oligonucleotide

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<210> 66
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 66
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<210> 67
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oligonucleotide

<400> 67
gctctgttag cttttagaa 20

<210> 68
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<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 68
ataagtgtga gctctgttag 20

<210> 69
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oligonucleotide

<400> 69
ggccccgag ataagtgtga 20

<210> 70
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 70
tcccttgccg ggtccccgag 20

<210> 71
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 71
gatctcgttc tcccttgccg 20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 72
tgttagggaa gatctcgttc 20

<210> 73
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 73
aactgcagca tgttagggaa 20

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 74
agctcctgca aactgcagca 20

<210> 75
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 75
 gaatcccgca agctcctgca

20

<210> 76
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 76
 ctcgcagctg gaatcccgca

20

<210> 77
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 77
 cttcgtcact ctcgcagctg

20

<210> 78
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 78
 gttcttcttt cttcgtcact

20

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 79
gcttctcgga gttcttcttt 20

<210> 80
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 80
tgtctgaata gcttctcgga 20

<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 81
tatccagcat tgtctgaata 20

<210> 82
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 82
gggccaggtg tatccagcat 20

<210> 83
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 83
 caacaggtac ggtccaggtg

20

<210> 84
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 84
 agatgacatc caacaggtac

20

<210> 85
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 85
 gtcattgcaat ggggaagatcg g

21

<210> 86
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 86
 ccgatcttcc cattgcatga c

21

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 87
gtcatgcaat tggaagatcg g

21

<210> 88
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 88
ccgatcttcc aattgcatga c

21

<210> 89
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 89
tacatctttg aaagtgcc

19

<210> 90
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 90
ggcgtttggt gttagggttg a

21

<210> 91
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 91
cgtctgggaa caaccaaaag t 21

<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 92
ggaaagctcg aggctttcgc t 21

<210> 93
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 93
atcaccagct tcattctctca gt 22

<210> 94
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 94
ggaaagctcg aggcgtttgc g 21

<210> 95
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 95
gtgttaccga tgatcc 16

<210> 96
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 96
gggatggtca tgcaat 16

<210> 97
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 97
caagtgggtgg 10

<210> 98
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 98
caaatgggtgg 10

<210> 99
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 99
 gggaagatc

9

<210> 100
 <211> 9
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 100
 tggaagatc

9

<210> 101
 <211> 655
 <212> PRT
 <213> Brassica napus

<220>
 <221> MOD_RES
 <222> (268)..(268)
 <223> Variable amino acid

<400> 101
 Met Ala Ala Ala Thr Ser Ser Ser Pro Ile Ser Leu Thr Ala Lys Pro
 1 5 10 15
 Ser Ser Lys Ser Pro Leu Pro Ile Ser Arg Phe Ser Leu Pro Phe Ser
 20 25 30
 Leu Thr Pro Gln Lys Asp Ser Ser Arg Leu His Arg Pro Leu Ala Ile
 35 40 45
 Ser Ala Val Leu Asn Ser Pro Val Asn Val Ala Pro Pro Ser Pro Glu
 50 55 60
 Lys Thr Asp Lys Asn Lys Thr Phe Val Ser Arg Tyr Ala Pro Asp Glu
 65 70 75 80
 Pro Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly
 85 90 95

Val Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His
 100 105 110
 Gln Ala Leu Thr Arg Ser Ser Thr Ile Arg Asn Val Leu Pro Arg His
 115 120 125
 Glu Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly
 130 135 140
 Lys Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu
 145 150 155 160
 Val Ser Gly Leu Ala Asp Ala Met Leu Asp Ser Val Pro Leu Val Ala
 165 170 175
 Ile Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln
 180 185 190
 Glu Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr
 195 200 205
 Leu Val Met Asp Val Asp Asp Ile Pro Arg Ile Val Gln Glu Ala Phe
 210 215 220
 Phe Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro
 225 230 235 240
 Lys Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Asp Gln Pro Met
 245 250 255
 Arg Leu Pro Gly Tyr Met Ser Arg Leu Pro Gln Xaa Pro Glu Val Ser
 260 265 270
 Gln Leu Gly Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Arg Pro Val
 275 280 285
 Leu Tyr Val Gly Gly Gly Ser Leu Asn Ser Ser Glu Glu Leu Gly Arg
 290 295 300
 Phe Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu
 305 310 315 320
 Gly Ser Tyr Pro Cys Asn Asp Glu Leu Ser Leu Gln Met Leu Gly Met
 325 330 335
 His Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu
 340 345 350
 Leu Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu
 355 360 365
 Ala Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala
 370 375 380

Glu Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val
 385 390 395 400
 Lys Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu
 405 410 415
 Glu Leu Lys Leu Asp Phe Gly Val Trp Arg Ser Glu Leu Ser Glu Gln
 420 425 430
 Lys Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro
 435 440 445
 Pro Gln Tyr Ala Ile Gln Ile Leu Asp Glu Leu Thr Glu Gly Lys Ala
 450 455 460
 Ile Ile Ser Thr Gly Val Gly Gln Arg Gln Met Trp Ala Ala Gln Phe
 465 470 475 480
 Tyr Lys Tyr Arg Lys Pro Arg Gln Trp Leu Ser Ser Ser Gly Leu Gly
 485 490 495
 Ala Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn
 500 505 510
 Pro Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met
 515 520 525
 Asn Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys
 530 535 540
 Ile Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu
 545 550 555 560
 Asp Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Tyr Leu Gly Asp Pro
 565 570 575
 Ala Arg Glu Asn Glu Ile Phe Pro Asn Met Leu Gln Phe Ala Gly Ala
 580 585 590
 Cys Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Glu Glu Leu Arg Glu
 595 600 605
 Ala Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val
 610 615 620
 Ile Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly
 625 630 635 640
 Thr Phe Lys Asp Val Ile Thr Glu Gly Asp Gly Arg Thr Lys Tyr
 645 650 655

<210> 102
 <211> 652
 <212> PRT
 <213> Brassica napus

<220>
 <221> MOD_RES
 <222> (464)..(464)
 <223> Variable amino acid

<400> 102

Met	Ala	Ala	Ala	Thr	Ser	Ser	Ser	Pro	Ile	Ser	Leu	Thr	Ala	Lys	Pro	1	5	10	15
Ser	Ser	Lys	Ser	Pro	Leu	Pro	Ile	Ser	Arg	Phe	Ser	Leu	Pro	Phe	Ser	20	25	30	
Leu	Thr	Pro	Gln	Lys	Pro	Ser	Ser	Arg	Leu	His	Arg	Pro	Leu	Ala	Ile	35	40	45	
Ser	Ala	Val	Leu	Asn	Ser	Pro	Val	Asn	Val	Ala	Pro	Glu	Lys	Thr	Asp	50	55	60	
Lys	Ile	Lys	Thr	Phe	Ile	Ser	Arg	Tyr	Ala	Pro	Asp	Glu	Pro	Arg	Lys	65	70	75	80
Gly	Ala	Asp	Ile	Leu	Val	Glu	Ala	Leu	Glu	Arg	Gln	Gly	Val	Glu	Thr	85	90	95	
Val	Phe	Ala	Tyr	Pro	Gly	Gly	Ala	Ser	Met	Glu	Ile	His	Gln	Ala	Leu	100	105	110	
Thr	Arg	Ser	Ser	Thr	Ile	Arg	Asn	Val	Leu	Pro	Arg	His	Glu	Gln	Gly	115	120	125	
Gly	Val	Phe	Ala	Ala	Glu	Gly	Tyr	Ala	Arg	Ser	Ser	Gly	Lys	Pro	Gly	130	135	140	
Ile	Cys	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	Ser	Gly	145	150	155	160
Leu	Ala	Asp	Ala	Met	Leu	Asp	Ser	Val	Pro	Leu	Val	Ala	Ile	Thr	Gly	165	170	175	
Gln	Val	Pro	Arg	Arg	Met	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Thr	Pro	180	185	190	
Ile	Val	Glu	Val	Thr	Arg	Ser	Ile	Thr	Lys	His	Asn	Tyr	Leu	Val	Met	195	200	205	
Asp	Val	Asp	Asp	Ile	Pro	Arg	Ile	Val	Gln	Glu	Ala	Phe	Phe	Leu	Ala	210	215	220	

Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys Asp Ile
 225 230 235 240
 Gln Gln Gln Leu Ala Ile Pro Asn Trp Asp Gln Pro Met Arg Leu Pro
 245 250 255
 Gly Tyr Met Ser Arg Leu Pro Gln Pro Pro Glu Val Ser Gln Leu Gly
 260 265 270
 Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Arg Pro Val Leu Tyr Val
 275 280 285
 Gly Gly Gly Ser Leu Asn Ser Ser Glu Glu Leu Gly Arg Phe Val Glu
 290 295 300
 Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ser Tyr
 305 310 315 320
 Pro Cys Asn Asp Glu Leu Ser Leu Gln Met Leu Gly Met His Gly Thr
 325 330 335
 Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu Ala Phe
 340 345 350
 Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala Phe Ala
 355 360 365
 Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly
 370 375 380
 Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys Leu Ala
 385 390 395 400
 Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu Leu Lys
 405 410 415
 Leu Asp Phe Gly Val Trp Arg Ser Glu Leu Ser Glu Gln Lys Gln Lys
 420 425 430
 Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro Gln Tyr
 435 440 445
 Ala Ile Gln Val Leu Asp Glu Leu Thr Gln Gly Lys Ala Ile Ile Xaa
 450 455 460
 Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr
 465 470 475 480
 Arg Lys Pro Arg Gln Trp Leu Ser Ser Ser Gly Leu Gly Ala Met Gly
 485 490 495
 Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro Asp Ala
 500 505 510

Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln
515 520 525

Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Ile Leu Leu
530 535 540

Leu Asn Asn Gln His Leu Gly Met Val Met Gln Leu Glu Asp Arg Phe
545 550 555 560

Tyr Lys Ala Asn Arg Ala His Thr Tyr Leu Gly Asp Pro Ala Arg Glu
565 570 575

Asn Glu Ile Phe Pro Asn Met Leu Gln Phe Ala Gly Ala Cys Gly Ile
580 585 590

Pro Ala Ala Arg Val Thr Lys Lys Glu Glu Leu Arg Glu Ala Ile Gln
595 600 605

Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Ala Ile Cys Pro
610 615 620

His Gln Glu His Val Leu Pro Met Ile Pro Ser Gly Gly Thr Phe Lys
625 630 635 640

Asp Val Ile Thr Glu Gly Asp Gly Arg Thr Lys Tyr
645 650

<210> 103

<211> 655

<212> PRT

<213> Brassica napus

<400> 103

Met Ala Ala Ala Thr Ser Ser Ser Pro Ile Ser Leu Thr Ala Lys Pro
1 5 10 15

Ser Ser Lys Ser Pro Leu Pro Ile Ser Arg Phe Ser Leu Pro Phe Ser
20 25 30

Leu Thr Pro Gln Lys Asp Ser Ser Arg Leu His Arg Pro Leu Ala Ile
35 40 45

Ser Ala Val Leu Asn Ser Pro Val Asn Val Ala Pro Pro Ser Pro Glu
50 55 60

Lys Thr Asp Lys Asn Lys Thr Phe Val Ser Arg Tyr Ala Pro Asp Glu
65 70 75 80

Pro Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly
85 90 95

Val Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His
100 105 110

Gln Ala Leu Thr Arg Ser Ser Thr Ile Arg Asn Val Leu Pro Arg His
 115 120 125
 Glu Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly
 130 135 140
 Lys Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu
 145 150 155 160
 Val Ser Gly Leu Ala Asp Ala Met Leu Asp Ser Val Pro Leu Val Ala
 165 170 175
 Ile Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln
 180 185 190
 Glu Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr
 195 200 205
 Leu Val Met Asp Val Asp Asp Ile Pro Arg Ile Val Gln Glu Ala Phe
 210 215 220
 Phe Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro
 225 230 235 240
 Lys Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Asp Gln Pro Met
 245 250 255
 Arg Leu Pro Gly Tyr Met Ser Arg Leu Pro Gln Pro Pro Glu Val Ser
 260 265 270
 Gln Leu Gly Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Arg Pro Val
 275 280 285
 Leu Tyr Val Gly Gly Gly Ser Leu Asn Ser Ser Glu Glu Leu Gly Arg
 290 295 300
 Phe Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu
 305 310 315 320
 Gly Ser Tyr Pro Cys Asn Asp Glu Leu Ser Leu Gln Met Leu Gly Met
 325 330 335
 His Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu
 340 345 350
 Leu Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu
 355 360 365
 Ala Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala
 370 375 380
 Glu Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val
 385 390 395 400

Lys Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu
 405 410 415
 Glu Leu Lys Leu Asp Phe Gly Val Trp Arg Ser Glu Leu Ser Glu Gln
 420 425 430
 Lys Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro
 435 440 445
 Pro Gln Tyr Ala Ile Gln Ile Leu Asp Glu Leu Thr Glu Gly Lys Ala
 450 455 460
 Ile Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe
 465 470 475 480
 Tyr Lys Tyr Arg Lys Pro Arg Gln Trp Leu Ser Ser Ser Gly Leu Gly
 485 490 495
 Ala Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn
 500 505 510
 Pro Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met
 515 520 525
 Asn Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys
 530 535 540
 Ile Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu
 545 550 555 560
 Asp Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Tyr Leu Gly Asp Pro
 565 570 575
 Ala Arg Glu Asn Glu Ile Phe Pro Asn Met Leu Gln Phe Ala Gly Ala
 580 585 590
 Cys Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Glu Glu Leu Arg Glu
 595 600 605
 Ala Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val
 610 615 620
 Ile Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Ser Gly Gly
 625 630 635 640
 Thr Phe Lys Asp Val Ile Thr Glu Gly Asp Gly Arg Thr Lys Tyr
 645 650 655

<210> 104

<211> 652

<212> PRT

<213> Brassica napus

<400> 104

Met	Ala	Ala	Ala	Thr	Ser	Pro	Ser	Pro	Ile	Ser	Leu	Thr	Ala	Lys	Pro
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Ser	Ser	Lys	Ser	Pro	Leu	Pro	Ile	Ser	Arg	Phe	Ser	Leu	Pro	Phe	Ser
		20						25					30		
Leu	Thr	Pro	Gln	Lys	Pro	Ser	Ser	Arg	Leu	His	Arg	Pro	Leu	Ala	Ile
		35					40					45			
Ser	Ala	Val	Leu	Asn	Ser	Pro	Val	Asn	Val	Ala	Pro	Glu	Lys	Thr	Asp
	50					55					60				
Lys	Ile	Lys	Thr	Phe	Ile	Ser	Arg	Tyr	Ala	Pro	Asp	Glu	Pro	Arg	Lys
65					70					75					80
Gly	Ala	Asp	Ile	Leu	Val	Glu	Ala	Leu	Glu	Arg	Gln	Gly	Val	Glu	Thr
			85						90					95	
Val	Phe	Ala	Tyr	Pro	Gly	Gly	Ala	Ser	Met	Glu	Ile	His	Gln	Ala	Leu
			100					105					110		
Thr	Arg	Ser	Ser	Thr	Ile	Arg	Asn	Val	Leu	Pro	Arg	His	Glu	Gln	Gly
		115					120					125			
Gly	Val	Phe	Ala	Ala	Glu	Gly	Tyr	Ala	Arg	Ser	Ser	Gly	Lys	Pro	Gly
	130					135					140				
Ile	Cys	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	Ser	Gly
145					150					155					160
Leu	Ala	Asp	Ala	Met	Leu	Asp	Ser	Val	Pro	Leu	Val	Ala	Ile	Thr	Gly
				165					170					175	
Gln	Val	Pro	Arg	Arg	Met	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Thr	Pro
		180						185					190		
Ile	Val	Glu	Val	Thr	Arg	Ser	Ile	Thr	Lys	His	Asn	Tyr	Leu	Val	Met
		195					200					205			
Asp	Val	Asp	Asp	Ile	Pro	Arg	Ile	Val	Gln	Glu	Ala	Phe	Phe	Leu	Ala
	210					215					220				
Thr	Ser	Gly	Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Val	Pro	Lys	Asp	Ile
225					230					235					240
Gln	Gln	Gln	Leu	Ala	Ile	Pro	Asn	Trp	Asp	Gln	Pro	Met	Arg	Leu	Pro
			245						250					255	
Gly	Tyr	Met	Ser	Arg	Leu	Pro	Gln	Pro	Pro	Glu	Val	Ser	Gln	Leu	Gly
		260						265					270		

Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Arg Pro Val Leu Tyr Val
 275 280 285
 Gly Gly Gly Ser Leu Asn Ser Ser Glu Glu Leu Gly Arg Phe Val Glu
 290 295 300
 Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly Ser Tyr
 305 310 315 320
 Pro Cys Asn Asp Glu Leu Ser Leu Gln Met Leu Gly Met His Gly Thr
 325 330 335
 Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu Ala Phe
 340 345 350
 Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala Phe Ala
 355 360 365
 Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu Ile Gly
 370 375 380
 Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys Leu Ala
 385 390 395 400
 Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu Leu Lys
 405 410 415
 Leu Asp Phe Gly Val Trp Arg Ser Glu Leu Ser Glu Gln Lys Gln Lys
 420 425 430
 Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro Gln Tyr
 435 440 445
 Ala Ile Gln Val Leu Asp Glu Leu Thr Gln Gly Lys Ala Ile Ile Ser
 450 455 460
 Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr Lys Tyr
 465 470 475 480
 Arg Lys Pro Arg Gln Trp Leu Ser Ser Ser Gly Leu Gly Ala Met Gly
 485 490 495
 Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro Asp Ala
 500 505 510
 Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn Val Gln
 515 520 525
 Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Ile Leu Leu
 530 535 540
 Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp Arg Phe
 545 550 555 560

Tyr Lys Ala Asn Arg Ala His Thr Tyr Leu Gly Asp Pro Ala Arg Glu
 565 570 575
 Asn Glu Ile Phe Pro Asn Met Leu Gln Phe Ala Gly Ala Cys Gly Ile
 580 585 590
 Pro Ala Ala Arg Val Thr Lys Lys Glu Glu Leu Arg Glu Ala Ile Gln
 595 600 605
 Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile Cys Pro
 610 615 620
 His Gln Glu His Val Leu Pro Met Ile Pro Ser Gly Gly Thr Phe Glu
 625 630 635 640
 Asp Val Ile Thr Glu Gly Asp Gly Arg Thr Lys Tyr
 645 650

<210> 105
 <211> 10
 <212> PRT
 <213> Brassica napus

<400> 105
 Ile Pro Ser Gly Gly Thr Phe Lys Asp Val
 1 5 10

<210> 106
 <211> 30
 <212> DNA
 <213> Brassica napus

<400> 106
 atcccaagtg gtggcacttt caaagatgta 30

<210> 107
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 107
 catctttgaa agtgccacca c 21

<210> 108
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 108
 Ile Pro Asn Gly Gly Thr Phe Lys Asp Val
 1 5 10

<210> 109
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 109
 atcccaaagt gtggcacttt caaagatgta

30

<210> 110
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 110
 catctttgaa agtgccacca t

21

<210> 111
 <211> 10
 <212> PRT
 <213> Brassica napus

<400> 111
 Met Gln Trp Glu Asp Arg Phe Tyr Lys Ala
 1 5 10

<210> 112
 <211> 30
 <212> DNA
 <213> Brassica napus

<400> 112
atgcaatggg aagatcgggt ctacaaagct 30

<210> 113
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 113
ctttgtagaa ccgatcttcc c 21

<210> 114
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 114
Met Gln Leu Glu Asp Arg Phe Tyr Lys Ala
1 5 10

<210> 115
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 115
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<210> 116
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 116
ctttgtagaa ccgatcttcc a